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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,071

DATE: 03/28/2002

TIME: 15:51:40

Input Set : A:\07334-335001.TXT

Output Set: N:\CRF3\03282002\I931071.raw

4 <110> APPLICANT: Bertin, John
 5 Alnemri, Emad S.
 7 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 8 PROTEIN FAMILY AND USES THEREOF
 11 <130> FILE REFERENCE: 07334-335001
 13 <140> CURRENT APPLICATION NUMBER: 09/931,071
 C--> 14 <141> CURRENT FILING DATE: 2002-03-18
 16 <150> PRIOR APPLICATION NUMBER: 09/428,252
 17 <151> PRIOR FILING DATE: 1999-10-27
 19 <160> NUMBER OF SEQ ID NOS: 11
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5444
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (523)...(4809)
 32 <400> SEQUENCE: 1

33	gcccccaggc ctggagaggt ctgaagaaac ctgggagcca gcagccccggq gctccactct	60
34	ggttctgaa agcccatattcc ctgctctgcg gtcctccca ccccacctct tctcagccctt	120
35	gcagctcaag gggtatctc aggagtccag gaccaggag aggaaagaat ctgaggaaca	180
36	cagaacagtg agcggttgc cc acacccatc tcccttcacc acatctcccc tcaccctcac	240
37	cctccctgcc tggcccttggaa ccccatccca ggacctccct atcagctgac ttcttccagt	300
38	gtcttcaggcccctctggg ctcctccctc ccctggcttt tccttaccact cccctcttat	360
39	cggcgtctat ctgttaggtgc cctgggattt ataaaactgg gttccgaatg ctgaataaga	420
40	gacggttaaga gccaaggcaa aggacagcac ttttctctgc ctgcctgata ccctcaccac	480
41	ctgggaacat ccccccagaca ccctttaac tccgggacag ag atg gct ggc gga	534
42	Met Ala Gly Gly	
43	1	
45	gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg aag aag gag gag	582
46	Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu Lys Lys Glu Glu	
47	5 10 15 20	
49	ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg cac tcc agg agc	630
50	Leu Lys Glu Phe Gln Leu Leu Ala Asn Lys Ala His Ser Arg Ser	
51	25 30 35	
53	tct tcg ggt gag aca ccc gct cag cca gag aag acg agt ggc atg gag	678
54	Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr Ser Gly Met Glu	
55	40 45 50	
57	gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag cgg gcc tgg gac	726
58	Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln Arg Ala Trp Asp	
59	55 60 65	
61	cta gcc ctc cat acc tgg gag cag atg ggg ctg agg tca ctg tgc gcc	774

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62	Leu	Ala	Leu	His	Thr	Trp	Glu	Gln	Met	Gly	Leu	Arg	Ser	Leu	Cys	Ala
63	70					75			80							
65	caa	gcc	cag	gaa	ggg	gca	ggc	cac	tct	ccc	tca	ttc	ccc	tac	agc	cca
66	Gln	Ala	Gln	Glu	Gly	Ala	Gly	His	Ser	Pro	Ser	Phe	Pro	Tyr	Ser	Pro
67	85					90			95							100
69	agt	gaa	ccc	cac	ctg	ggg	tct	ccc	agc	caa	ccc	acc	tcc	acc	gca	gtg
70	Ser	Glu	Pro	His	Leu	Gly	Ser	Pro	Ser	Gln	Pro	Thr	Ser	Thr	Ala	Val
71						105			110						115	
73	cta	atg	ccc	tgg	atc	cat	gaa	ttg	ccg	gcg	ggg	tgc	acc	cag	ggc	tca
74	Leu	Met	Pro	Trp	Ile	His	Glu	Leu	Pro	Ala	Gly	Cys	Thr	Gln	Gly	Ser
75						120			125						130	
77	gag	aga	agg	gtt	ttg	aga	cag	ctg	cct	gac	aca	tct	gga	cgc	cgc	tgg
78	Glu	Arg	Arg	Val	Leu	Arg	Gln	Leu	Pro	Asp	Thr	Ser	Gly	Arg	Arg	Trp
79						135			140						145	
81	aga	gaa	atc	tct	gcc	tca	ctc	ctc	tac	caa	gct	ctt	cca	agc	tcc	cca
82	Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu	Pro	Ser	Ser	Pro
83						150			155						160	
85	gac	cat	gag	tct	cca	agc	cag	gag	tca	ccc	aac	gcc	ccc	aca	tcc	aca
86	Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala	Pro	Thr	Ser	Thr
87	165					170			175						180	
89	gca	gtg	ctg	ggg	agc	tgg	gga	tcc	cca	cct	cag	ccc	agc	cta	gca	ccc
90	Ala	Val	Leu	Gly	Ser	Trp	Gly	Ser	Pro	Pro	Gln	Pro	Ser	Leu	Ala	Pro
91						185			190						195	
93	aga	gag	cag	gag	gct	cct	ggg	acc	caa	tgg	cct	ctg	gat	gaa	acg	tca
94	Arg	Glu	Gln	Glu	Ala	Pro	Gly	Thr	Gln	Trp	Pro	Leu	Asp	Glu	Thr	Ser
95						200			205						210	
97	gga	att	tac	tac	aca	gaa	atc	aga	gaa	aga	gag	aaa	tca	gag		1206
98	Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg	Glu	Lys	Ser	Glu
99						215			220						225	
101	aaa	ggc	agg	ccc	cca	tgg	gca	gcg	gtg	gta	gga	acg	ccc	cca	cag	gcg
102	Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr	Pro	Pro	Gln	Ala
103						230			235						240	
105	cac	acc	agc	cta	cag	ccc	cac	cac	cac	cca	tgg	gag	cct	tct	gtg	aga
106	His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu	Pro	Ser	Val	Arg
107	245					250			255						260	
109	gag	agc	ctc	tgt	tcc	aca	tgg	ccc	tgg	aaa	aat	gag	gat	ttt	aac	caa
110	Glu	Ser	Leu	Cys	Ser	Thr	Trp	Pro	Trp	Lys	Asn	Glu	Asp	Phe	Asn	Gln
111						265			270						275	
113	aaa	ttc	aca	cag	ctg	cta	ctt	cta	caa	aga	cct	cac	ccc	aga	agc	caa
114	Lys	Phe	Thr	Gln	Leu	Leu	Leu	Leu	Gln	Arg	Pro	His	Pro	Arg	Ser	Gln
115						280			285						290	
117	gat	ccc	ctg	gtc	aag	aga	agc	tgg	cct	gat	tat	gtg	gag	gag	aat	cga
118	Asp	Pro	Leu	Val	Lys	Arg	Ser	Trp	Pro	Asp	Tyr	Val	Glu	Glu	Asn	Arg
119						295			300						305	
121	gga	cat	tta	att	gag	atc	aga	gac	tta	ttt	ggc	cca	ggc	ctg	gat	acc
122	Gly	His	Leu	Ile	Glu	Ile	Arg	Asp	Leu	Phe	Gly	Pro	Gly	Leu	Asp	Thr
123						310			315						320	
125	caa	gaa	cct	cgc	ata	gtc	ata	ctg	cag	ggg	gct	gct	gga	att	ggg	aag
126	Gln	Glu	Pro	Arg	Ile	Val	Ile	Leu	Gln	Gly	Ala	Ala	Gly	Ile	Gly	Lys

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127	325	330	335	340	
129	tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg aga ggc cag ctg				1590
130	Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly Arg Gly Gln Leu				
131	345	350	355		
133	tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc tgc aga gag ctg				1638
134	Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser Cys Arg Glu Leu				
135	360	365	370		
137	gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc gga aaa gat ggg				1686
138	Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile Gly Lys Asp Gly				
139	375	380	385		
141	aca gcc act ccg gct ccc att aga cag atc ctg tct agg cca gag cgg				1734
142	Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser Arg Pro Glu Arg				
143	390	395	400		
145	ctg ctc ttc atc ctc gat ggt gta gat gag cca gga tgg gtc ttg cag				1782
146	Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly Trp Val Leu Gln				
147	405	410	415	420	
149	gag ccg agt tct gag ctc tgt ctg cac tgg agc cag cca cag ccg gcg				1830
150	Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln Pro Gln Pro Ala				
151	425	430	435		
153	gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata ctt ccc gag gca				1878
154	Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile Leu Pro Glu Ala				
155	440	445	450		
157	tcc ttc ctg atc acg gct cgg acc aca gct ctg cag aac ctc att cct				1926
158	Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln Asn Leu Ile Pro				
159	455	460	465		
161	tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg ttc tct gag tcc				1974
162	Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly Phe Ser Glu Ser				
163	470	475	480		
165	agc agg aag gaa tat ttc tac aga tat ttc aca gat gaa agg caa gca				2022
166	Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp Glu Arg Gln Ala				
167	485	490	495	500	
169	att aga gcc ttt agg ttg gtc aaa tca aac aaa gag ctc tgg gcc ctg				2070
170	Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu Leu Trp Ala Leu				
171	505	510	515		
173	tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act tgc ctg atg cag				2118
174	Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr Cys Leu Met Gln				
175	520	525	530		
177	cag atg aag cgg aag gaa aaa ctc aca ctg act tcc aag acc acc aca				2166
178	Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser Lys Thr Thr Thr				
179	535	540	545		
181	acc ctc tgt cta cat tac ctt gcc cag gct ctc caa gct cag cca ttg				2214
182	Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln Ala Gln Pro Leu				
183	550	555	560		
185	gga ccc cag ctc aga gac ctc tgc tct ctg gct gct gag ggc atc tgg				2262
186	Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala Glu Gly Ile Trp				
187	565	570	575	580	
189	caa aaa aag acc ctt ttc agt cca gat gac ctc agg aag cat ggg tta				2310
190	Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg Lys His Gly Leu				
191	585	590	595		

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193 gat	ggg	gcc	atc	atc	tcc	acc	ttc	ttg	aag	atg	ggt	att	ctt	caa	gag		2358
194 Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly	Ile	Ile	Gln	Glu		
195		600					605						610				
197 cac	ccc	atc	cct	ctg	agc	tac	agc	ttc	att	cac	ctc	tgt	ttc	caa	gag		2406
198 His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	Cys	Phe	Gln	Glu		
199		615					620					625					
201 ttc	ttt	gca	gca	atg	tcc	tat	gtc	ttg	gag	gat	gag	aag	ggg	aga	ggt		2454
202 Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu	Lys	Gly	Arg	Gly		
203		630					635					640					
205 aaa	cat	tct	aat	tgc	atc	ata	gat	ttg	gaa	aag	acg	cta	gaa	gca	tat		2502
206 Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr	Leu	Glu	Ala	Tyr		
207	645				650					655			660				
209 gga	ata	cat	ggc	ctg	ttt	ggg	gca	tca	acc	aca	cgt	ttc	cta	ttg	ggc		2550
210 Gly	Ile	His	Gly	Leu	Phe	Gly	Ala	Ser	Thr	Thr	Arg	Phe	Leu	Leu	Gly		
211		665					670					675					
213 ctg	tta	agt	gat	ggg	gag	aga	gag	atg	gag	aac	atc	ttt	cac	tgc		2598	
214 Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn	Ile	Phe	His	Cys		
215		680					685					690					
217 cgg	ctg	tct	cag	ggg	agg	aac	ctg	atg	cag	tgg	gtc	ccg	tcc	ctg	cag		2646
218 Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	Pro	Ser	Leu	Gln		
219		695					700					705					
221 ctg	ctg	ctg	cag	cca	cac	tct	ctg	gag	tcc	ctc	cac	tgc	ttg	tac	gag		2694
222 Leu	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His	Cys	Leu	Tyr	Glu		
223		710					715					720					
225 act	cgg	aac	aaa	acg	ttc	ctg	aca	caa	gtg	atg	gcc	cat	ttc	gaa	gaa		2742
226 Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	His	Phe	Glu			
227	725				730					735			740				
229 atg	ggc	atg	tgt	gtt	gaa	aca	gac	atg	gag	ctc	tta	gtg	tgc	act	ttc		2790
230 Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	Val	Cys	Thr	Phe		
231		745					750					755					
233 tgc	att	aaa	ttc	agc	cgc	cac	gtg	aag	aag	ctt	cag	ctg	att	gag	ggc		2838
234 Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	Leu	Ile	Glu	Gly		
235		760					765					770					
237 agg	cag	cac	aga	tca	aca	tgg	agc	ccc	acc	atg	gta	gtc	ctg	ttc	agg		2886
238 Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	Val	Leu	Phe	Arg		
239		775					780					785					
241 tgg	gtc	cca	gtc	aca	gat	gcc	tat	tgg	cag	att	ctc	ttc	tcc	gtc	ctc		2934
242 Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	Phe	Ser	Val	Leu		
243		790					795					800					
245 aag	gtc	acc	aga	aac	ctg	aag	gag	ctg	gac	cta	agt	gga	aac	tcg	ctg		2982
246 Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	Gly	Asn	Ser	Leu		
247	805				810					815			820				
249 agc	cac	tct	gca	gtg	aag	agt	ctt	tgt	aag	acc	ctg	aga	cgc	cct	cgc		3030
250 Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	Arg	Arg	Pro	Arg		
251		825					830					835					
253 tgc	ctc	ctg	gag	acc	ctg	cgg	ttt	gct	ggc	tgt	ggc	ctc	aca	gct	gag		3078
254 Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	Leu	Thr	Ala	Glu		
255		840					845					850					
257 gac	tgc	aag	gac	ctt	gcc	ttt	ggg	ctg	aga	gcc	aac	cag	acc	ctg	acc		3126

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258 Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn Gln Thr Leu Thr		
259 855 860 865		
261 gag ctg gac ctg agc ttc aat gtg ctc acg gat gct gga gcc aaa cac		3174
262 Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala Gly Ala Lys His		
263 870 875 880		
265 ctt tgc cag aga ctg aga cag ccg agc tgc aag cta cag cga ctg cag		3222
266 Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu Gln Arg Leu Gln		
267 885 890 895 900		
269 ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag gac ctg gcc tct		3270
270 Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln Asp Leu Ala Ser		
271 905 910 915		
273 gtg ctt agt gcc agc ccc agc ctg aag gag cta gac ctg cag cag aac		3318
274 Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp Leu Gln Gln Asn		
275 920 925 930		
277 aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag ggg ctc agg cat		3366
278 Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu Gly Leu Arg His		
279 935 940 945		
281 cct gcc tgc aaa ctc ata cgc ctg ggg ctg gac cag aca act ctg agt		3414
282 Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln Thr Thr Leu Ser		
283 950 955 960		
285 gat gag atg agg cag gaa ctg agg gcc ctg gag cag gag aaa cct cag		3462
286 Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln Glu Lys Pro Gln		
287 965 970 975 980		
289 ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg acc cct act gag		3510
290 Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met Thr Pro Thr Glu		
291 985 990 995		
293 ggc ctg gat acg gga gag atg agt aat agc aca tcc tca ctc aag cgg		3558
294 Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser Ser Leu Lys Arg		
295 1000 1005 1010		
297 cag aga ctc gga tca gag agg gcg gct tcc cat gtt gct cag gct aat		3606
298 Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val Ala Gln Ala Asn		
299 1015 1020 1025		
301 ctc aaa ctc ctg gac gtg agc aag atc ttc cca att gct gag att gca		3654
302 Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile Ala Glu Ile Ala		
303 1030 1035 1040		
305 gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc ttg tgc gtg cct		3702
306 Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu Leu Cys Val Pro		
307 1045 1050 1055 1060		
309 tct cct gcc tct caa ggg gac ctg cat acg aag cct ttg ggg act gac		3750
310 Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro Leu Gly Thr Asp		
311 1065 1070 1075		
313 gat gac ttc tgg ggc ccc acg ggg cct gtg gct act gag gta gtt gac		3798
314 Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr Glu Val Val Asp		
315 1080 1085 1090		
317 aaa gaa aag aac ttg tac cga gtt cac ttc cct gta gct ggc tcc tac		3846
318 Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val Ala Gly Ser Tyr		
319 1095 1100 1105		
321 cgc tgg ccc aac acg ggt ctc tgc ttt gtg atg aga gaa gcg gtg acc		3894
322 Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg Glu Ala Val Thr		

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date